

SEQ ID NO:50: Designed oligonucleotide primer to amplify JNK2 mRNA.

SEQ ID NO:51: Designed oligonucleotide primer to amplify Bax delta mRNA.

5 SEQ ID NO:52: Designed oligonucleotide primer to amplify Bax delta mRNA.

SEQ ID NO:53: Designed oligonucleotide primer to amplify BMK-1 mRNA.

10 SEQ ID NO:54: Designed oligonucleotide primer to amplify BMK-1 mRNA.

SEQ ID NO:55: Designed oligonucleotide primer to amplify BMK-2 mRNA.

SEQ ID NO:56: Designed oligonucleotide primer to amplify BMK-2 mRNA.

15 SEQ ID NO:57: Designed oligonucleotide primer to amplify Src-1 mRNA.

SEQ ID NO:58: Designed oligonucleotide primer to amplify Src-1 mRNA.

20 SEQ ID NO:59: Designed oligonucleotide primer to amplify p300/CBP mRNA.

SEQ ID NO:60: Designed oligonucleotide primer to amplify p300/CBP mRNA.

SEQ ID NO:61: Designed oligonucleotide primer to amplify β -actin mRNA.

25 SEQ ID NO:62: Designed oligonucleotide primer to

amplify β -actin mRNA.

CLAIMS

1. A method for detecting a gene that is influenced by an endocrine disruptor, characterized in which the method comprises:

preparing a nucleic acid sample containing mRNAs, or cDNAs therefor, derived from a cell, a tissue or an organism which has been exposed to a sample containing an endocrine disruptor;

hybridizing the nucleic acid sample with a DNA array onto which genes which are potentially influenced by the endocrine disruptor or DNA fragments derived from the genes which are potentially influenced by the endocrine disruptor are immobilized; and

selecting a gene that is influenced by the endocrine disruptor by comparing the results with results for a nucleic acid sample prepared using a control sample.

2. The method according to claim 1, wherein a gene selected from the group consisting of:

(1) a gene for a nuclear receptor or a gene related to nuclear receptor transcriptional coupling;

(2) a gene related to kinase-type signal transduction;

(3) a gene related to gonad differentiation;

(4) a gene for or related to a receptor-type